<110> Novartis AG

<120> Adenovirus particles with mutagenized fiber proteins

<130> 4-31452A

<160> 43

<170> PatentIn version 3.0

<210> 1
<211> 1746
<212> DNA
<213> Human adenovirus type 5

<220>
<221> CDS
<222> (1)..(1746)

<400> 1
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca   48
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1   5   10   15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc   96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
            20   25   30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct   1
                                                                       44
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
            35   40   45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc   1
                                                                       92
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
    50   55   60

```
aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc      2
40
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser

65                    70                   75                   80


caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac      2
88
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn

                 85                   90                   95


ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta      3
36
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu

             100                  105                  110


act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc      3
84
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr

         115                  120                  125


atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att      4
32
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile

     130                  135                  140


gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa      4
80
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln

145                  150                  155                  160


aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act      5
28
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
```

```
gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg    5
76
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
```
            180   185   190

```
aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg    6
24
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
```
        195   200   205

```
gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act    6
72
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
```
    210   215   220

```
ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act    7
20
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
```
225   230   235   240

```
gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca    7
68
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
```
                245   250   255

```
gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt    8
16
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
```
            260   265   270

```
agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag    8
64
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
```
                        Page 3

          275   280   285

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac   9
12
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn

     290   295   300

aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag   9
60
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu

305   310   315   320

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata   10
08
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile

               325   330   335

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca   10
56
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro

               340   345   350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat   11
04
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp

          355   360   365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac   11
52
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp

     370   375   380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act   12
00

```
      Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
      385                 390                 395                 400


      ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag   12
      48
      Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
                      405                 410                 415


      aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata   12
      96
      Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
                  420                 425                 430


      ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata   13
      44
      Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
                  435                 440                 445


      tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat   13
      92
      Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
              450                 455                 460


      gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt   14
      40
      Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
      465                 470                 475                 480


      aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga   14
      88
      Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
                      485                 490                 495


      ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc   15
```

36
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
            500   505   510

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa   15
84
Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
            515   520   525

cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac   16
32
Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
        530   535   540

aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc   16
80
Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
545   550   555   560

cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca   17
28
His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
                565   570   575

tac att gcc caa gaa taa   17
46
Tyr Ile Ala Gln Glu
                580

<210>   2
<211>   581
<212>   PRT
<213>   Human adenovirus type 5

<400>   2

```
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1               5               10              15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
            20              25              30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
        35              40              45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
    50              55              60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65              70              75              80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
            85              90              95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
        100             105             110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
    115             120             125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
    130             135             140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145             150             155             160

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
            165             170             175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
        180             185             190
```

Page 7

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
        195   200   205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
        210   215   220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225   230   235   240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
                245   250   255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
        260   265   270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
        275   280   285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
        290   295   300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305   310   315   320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
                325   330   335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
                340   345   350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
        355   360   365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
        370   375   380

```
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385                 390             395                     400


Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
                405             410                 415


Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
            420             425                 430


Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
        435             440                 445


Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
        450             455             460


Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465             470             475                     480


Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
            485             490                 495


Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
            500             505             510


Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
        515             520             525


Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
        530             535             540


Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
545             550             555                     560


His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
            565             570                 575
```

Tyr Ile Ala Gln Glu
         580

<210> 3
<211> 1746
<212> DNA
<213> Artificial

<220>
<223> Codes for a mutated Human Adenovirus type 5 fiber protein.

<220>
<221> CDS
<222> (1)..(1746)

<220>
<221> mutation
<222> (1222)..(1227)

<400> 3
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca   48
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1   5   10   15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc   96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
            20   25   30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct   144
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
        35   40   45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc   192
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
    50   55   60

```
aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc     2
40
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65                  70                  75                  80


caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac     2
88
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
                85                  90                  95


ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta     3
36
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
                100                 105                 110


act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc     3
84
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
        115                 120                 125


atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att     4
32
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
    130                 135                 140


gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa     4
80
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145                 150                 155                 160


aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act     5
28
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
```

```
                              165                   170                        175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg        5
76
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu

            180                   185                   190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg        6
24
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

        195                   200                   205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act        6
72
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr

    210                   215                   220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act        7
20
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr

225                   230                   235                   240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca        7
68
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala

                245                   250                   255

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt        8
16
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val

            260                   265                   270

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag        8
64
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
```

          275   280   285

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac   9
12
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn

     290   295   300

aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag   9
60
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu

305   310   315   320

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata   10
08
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile

               325   330   335

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca   10
56
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro

               340   345   350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat   11
04
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp

          355   360   365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac   11
52
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp

     370   375   380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act   12
00

```
     Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
     385                 390                 395                 400


     ttg tgg acc aca cca gct cca gag gct aac tgt aga cta aat gca gag     12
     48
     Leu Trp Thr Thr Pro Ala Pro Glu Ala Asn Cys Arg Leu Asn Ala Glu
                     405                 410                 415


     aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata     12
     96
     Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
                     420                 425                 430


     ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata     13
     44
     Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
                 435                 440                 445


     tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat     13
     92
     Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
             450                 455                 460


     gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt     14
     40
     Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
     465                 470                 475                 480


     aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga     14
     88
     Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
                     485                 490                 495


     ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc     15
```

36
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
        500   505   510

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa   15
84
Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
     515   520   525

cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac   16
32
Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
   530   535   540

aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc   16
80
Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
545   550   555   560

cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca   17
28
His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
        565   570   575

tac att gcc caa gaa taa   17
46
Tyr Ile Ala Gln Glu
       580

<210> 4
<211> 581
<212> PRT
<213> Artificial

<400> 4

```
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1               5                   10                  15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
            20                  25                  30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
        35                  40                  45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
    50                  55                  60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65                  70                  75                  80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
            85                  90                  95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
        100                 105                 110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
        115                 120                 125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
    130                 135                 140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145                 150                 155                 160

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
            165                 170                 175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
        180                 185                 190
```

Page 16

```
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
        195                 200                 205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
        210                 215                 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225                 230                 235                 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
                245                 250                 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
                260                 265                 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
        275                 280                 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
        290                 295                 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305                 310                 315                 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
                325                 330                 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
                340                 345                 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
        355                 360                 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
        370                 375                 380
```

```
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385             390             395                 400


Leu Trp Thr Thr Pro Ala Pro Glu Ala Asn Cys Arg Leu Asn Ala Glu
                405             410                 415


Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
            420             425             430


Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
        435             440             445


Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
    450             455             460


Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465             470             475                 480


Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
            485             490                 495


Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
            500             505             510


Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
        515             520             525


Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
    530             535             540


Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
545             550             555                 560


His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
            565             570             575
```

Tyr Ile Ala Gln Glu
            580

<210>   5
<211>   1740
<212>   DNA
<213>   Artificial

<220>
<223>   Codes for a mutated Human Adenovirus type 5 fiber protein.   Nuc
le
        otides corresponding to amino acids 441(V) & 442(K) of wild-typ
e
        fiber were deleted

<220>
<221>   CDS
<222>   (1)..(1740)

<400>   5
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca
48
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1   5   10   15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc
96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

            20   25   30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct   1
44
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

        35   40   45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc   1
92
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu

    50   55   60

```
aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc     2
40
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65              70              75              80


caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac     2
88
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
                85              90              95


ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta     3
36
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
            100             105             110


act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc     3
84
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
        115             120             125


atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att     4
32
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
    130             135             140


gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa     4
80
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145             150             155             160


aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act     5
28
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
```

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg   5
76
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu

            180   185   190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg   6
24
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

        195   200   205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act   6
72
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr

    210   215   220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act   7
20
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr

225   230   235   240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca   7
68
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala

            245   250   255

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt   8
16
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val

            260   265   270

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag   8
64
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln

                275   280   285

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac   9
12
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn

      290   295   300

aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag   9
60
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu

305   310   315   320

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata   10
08
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile

                325   330   335

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca   10
56
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro

                340   345   350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat   11
04
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp

      355   360   365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac   11
52
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp

      370   375   380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act   12
00

```
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385                 390                 395                 400


ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag      12
48
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
                405                 410                 415


aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata      12
96
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
                420                 425                 430


ctt gct aca gtt tca gtt ttg gcc ggc agt ttg gct cca ata tct gga      13
44
Leu Ala Thr Val Ser Val Leu Ala Gly Ser Leu Ala Pro Ile Ser Gly
            435                 440                 445


aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat gga gtg      13
92
Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val
        450                 455                 460


cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt aga aat      14
40
Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn
465                 470                 475                 480


gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga ttt atg      14
88
Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met
                485                 490                 495


cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc aaa agt      15
```

36
Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser
            500   505   510

aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa cct gta   15
84
Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val
        515   520   525

aca cta acc att aca cta aac ggt aca cag gaa aca gga gac aca act   16
32
Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr
    530   535   540

cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc cac aac   16
80
Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn
545   550   555   560

tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca tac att   17
28
Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile
                565   570   575

gcc caa gaa taa   17
40
Ala Gln Glu

<210>   6
<211>   579
<212>   PRT
<213>   Artificial

<400>   6

Page 24

```
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1               5                   10                  15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
            20                  25                  30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
        35                  40                  45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
    50                  55                  60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65                  70                  75                  80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
            85                  90                  95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
        100                 105                 110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
        115                 120                 125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
    130                 135                 140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145                 150                 155                 160

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
            165                 170                 175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
        180                 185                 190
```

Page 25

```
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
        195                 200                 205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
        210                 215                 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225                 230                 235                 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
                245                 250                 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
            260                 265                 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
        275                 280                 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
        290                 295                 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305                 310                 315                 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
                325                 330                 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
            340                 345                 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
        355                 360                 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
        370                 375                 380
```

Page 26

```
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385                 390                 395                 400


Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
                405                 410                 415


Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
            420                 425                 430


Leu Ala Thr Val Ser Val Leu Ala Gly Ser Leu Ala Pro Ile Ser Gly
            435                 440                 445


Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val
        450                 455                 460


Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn
465                 470                 475                 480


Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met
                485                 490                 495


Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser
            500                 505                 510


Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val
        515                 520                 525


Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr
        530                 535                 540


Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn
545                 550                 555                 560


Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile
                565                 570                 575
```

Ala Gln Glu

<210> 7
<211> 1740
<212> DNA
<213> Artificial

<220>
<223> Codes for a mutated Human Adenovirus type 5 fiber protein. Comb
in
       ation of the mutant fiber encoded in Seq ID: #3 & 5

<220>
<221> CDS
<222> (1)..(1740)

<400> 7
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca   48
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1   5   10   15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc   96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
                20   25   30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct   1
44
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
        35   40   45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc   1
92
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
    50   55   60

```
aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc        2
40
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65                     70                  75                  80


caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac        2
88
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
                   85                  90                  95


ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta        3
36
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
               100                 105                 110


act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc        3
84
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
           115                 120                 125


atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att        4
32
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
       130                 135                 140


gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa        4
80
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145                 150                 155                 160


aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act        5
28
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
               165                 170                 175
```

```
gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg      5
76
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
            180                 185                 190


aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg      6
24
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
            195                 200                 205


gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act      6
72
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
        210                 215                 220


ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act      7
20
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225                 230                 235                 240


gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca      7
68
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
                245                 250                 255


gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt      8
16
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
                260                 265                 270


agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag      8
64
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
            275                 280                 285
```

```
ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac    9
12
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
    290                 295                 300


aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag    9
60
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu

305                 310                 315                 320


gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata   10
08
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
                325                 330                 335


gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca   10
56
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
                340                 345                 350


aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat   11
04
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
        355                 360                 365


tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac   11
52
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
    370                 375                 380


agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act   12
00
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
```

```
385                      390                      395                      400

ttg tgg acc aca cca gct cca gag gct aac tgt aga cta aat gca gag    12
                                                                   48
Leu Trp Thr Thr Pro Ala Pro Glu Ala Asn Cys Arg Leu Asn Ala Glu
                 405                410                415


aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata    12
                                                                   96
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
                 420                425                430


ctt gct aca gtt tca gtt ttg gcc ggc agt ttg gct cca ata tct gga    13
                                                                   44
Leu Ala Thr Val Ser Val Leu Ala Gly Ser Leu Ala Pro Ile Ser Gly
                 435                440                445


aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat gga gtg    13
                                                                   92
Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val
             450                455                460


cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt aga aat    14
                                                                   40
Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn
465                470                475                480


gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga ttt atg    14
                                                                   88
Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met
                 485                490                495


cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc aaa agt    15
                                                                   36
Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser
```

```
          500                      505                      510

aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa cct gta    15
84
Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val

          515                      520                      525

aca cta acc att aca cta aac ggt aca cag gaa aca gga gac aca act    16
32
Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr

          530                      535                      540

cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc cac aac    16
80
Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn

545                      550                      555                      560

tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca tac att    17
28
Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile

                     565                      570                      575

gcc caa gaa taa                                                    17
40
Ala Gln Glu


<210>  8
<211>  579
<212>  PRT
<213>  Artificial

<400>  8

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
```

```
1                     5                     10                          15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
            20                  25                  30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
        35                  40                  45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
    50                  55                  60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65                  70                  75                      80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
                85                  90                  95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
            100                 105                 110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
        115                 120                 125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
    130                 135                 140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145                 150                 155                     160

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
            165                 170                 175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
        180                 185                 190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
```

195   200   205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
    210   215   220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225   230   235   240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
            245   250   255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
            260   265   270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
        275   280   285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
    290   295   300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305   310   315   320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
            325   330   335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
            340   345   350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
        355   360   365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
    370   375   380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
                            Page 35

385   390   395   400

Leu Trp Thr Thr Pro Ala Pro Glu Ala Asn Cys Arg Leu Asn Ala Glu
                405   410   415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
                420   425   430

Leu Ala Thr Val Ser Val Leu Ala Gly Ser Leu Ala Pro Ile Ser Gly
        435   440   445

Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val
        450   455   460

Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn
465   470   475   480

Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met
                485   490   495

Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser
        500   505   510

Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val
        515   520   525

Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr
        530   535   540

Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn
545   550   555   560

Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile
                565   570   575

Ala Gln Glu

```
<210>  9
<211>  1743
<212>  DNA
<213>  Artificial

<220>
<223>  Codes for a mutated Human Adenovirus type 5 fiber protein.  Nuc
le
       otides corresponding to amino acid 441(V) of wild-type fiber wa
s
       deleted

<220>
<221>  CDS
<222>  (1)..(1743)

<400>  9
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca
48
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1               5                   10                  15


tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc
96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
            20                  25                  30


ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct      1
44
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
        35                  40                  45


ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc      1
92
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
    50                  55                  60
```

```
aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc      2
40
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65                    70                  75                  80


caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac      2
88
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
                 85                  90                  95


ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta      3
36
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
             100                 105                 110


act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc      3
84
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
         115                 120                 125


atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att      4
32
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
     130                 135                 140


gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa      4
80
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145                 150                 155                 160


aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act      5
28
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
                 165                 170                 175
```

Page 38

```
gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg    5
76
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu

            180                 185                 190


aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg    6
24
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

        195                 200                 205


gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act    6
72
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr

    210                 215                 220


ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act    7
20
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr

225                 230                 235                 240


gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca    7
68
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala

                245                 250                 255


gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt    8
16
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val

            260                 265                 270


agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag    8
64
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln

        275                 280                 285
```

```
ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac     9
12
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
    290             295             300


aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag     9
60
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305             310             315             320


gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata    10
08
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
            325             330             335


gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca    10
56
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
            340             345             350


aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat    11
04
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
        355             360             365


tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac    11
52
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
    370             375             380


agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act    12
00
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
```

4-31452A.ST25.txt

```
       385                      390                      395                      400

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag       12
48
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
                  405                      410                      415


aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata       12
96
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
                  420                      425                      430


ctt gct aca gtt tca gtt ttg gct aaa ggc agt ttg gct cca ata tct       13
44
Leu Ala Thr Val Ser Val Leu Ala Lys Gly Ser Leu Ala Pro Ile Ser
            435                      440                      445


gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat gga       13
92
Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly
         450                      455                      460


gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt aga       14
40
Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg

465                      470                      475                      480


aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga ttt       14
88
Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe
                  485                      490                      495


atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc aaa       15
36
Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys
```

Page 41

```
                500                   505                    510


agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa cct      15
84
Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro

        515                   520                   525


gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac aca      16
32
Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr

      530                   535                   540


act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc cac      16
80
Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His

545                   550                   555                   560


aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca tac      17
28
Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr

                565                   570                   575


att gcc caa gaa taa                                                  17
43
Ile Ala Gln Glu

            580



<210>  10
<211>  580
<212>  PRT
<213>  Artificial

<400>  10

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
```

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
            20   25   30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
            35   40   45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
        50   55   60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65   70   75   80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
                85   90   95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
            100   105   110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
            115   120   125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
        130   135   140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145   150   155   160

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
            165   170   175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
            180   185   190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

```
              195                    200                          205

    Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
        210                    215                220

    Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
    225                    230                235                    240

    Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
                245                    250                255

    Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
                260                    265                270

    Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
                275                    280                285

    Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
        290                    295                300

    Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
    305                    310                315                    320

    Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
                325                    330                335

    Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
                340                    345                350

    Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
        355                    360                365

    Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
        370                    375                380

    Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
```

Page 44

385   390   395   400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
                    405   410   415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
                420   425   430

Leu Ala Thr Val Ser Val Leu Ala Lys Gly Ser Leu Ala Pro Ile Ser
            435   440   445

Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly
        450   455   460

Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg
465   470   475   480

Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe
                485   490   495

Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys
            500   505   510

Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro
            515   520   525

Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr
        530   535   540

Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His
545   550   555   560

Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr
                565   570   575

Ile Ala Gln Glu

```
<210>  11
<211>  1743
<212>  DNA
<213>  Artificial

<220>
<223>  Codes for a mutated Human Adenovirus type 5 fiber protein.  Nucle
       otides corresponding to amino acid 442(K) of wild-type fiber wa
s
       deleted

<220>
<221>  CDS
<222>  (1)..(1743)

<400>  11
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca       48
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1               5                   10                  15


tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc       96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
                20                  25                  30


ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct      1
                                                                      44
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
        35                  40                  45


ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc      1
                                                                      92
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
    50                  55                  60
```

```
aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc       2
40
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser

65                    70                   75                   80


caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac       2
88
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn

                 85                   90                   95


ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta       3
36
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu

             100                  105                  110


act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc       3
84
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr

         115                  120                  125


atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att       4
32
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile

     130                  135                  140


gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa       4
80
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln

145                  150                  155                  160


aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act       5
28
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr

             165                  170                  175
```

Page 47

```
gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg        5
76
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
             180              185              190


aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg        6
24
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
         195              200              205


gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act        6
72
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
     210              215              220


ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act        7
20
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225              230              235              240


gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca        7
68
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
             245              250              255


gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt        8
16
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
             260              265              270


agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag        8
64
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
         275              280              285
```

```
ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac       9
12
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
     290                 295                 300


aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag       9
60
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu

305                 310                 315                 320


gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata      10
08
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
                 325                 330                 335


gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca      10
56
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
                 340                 345                 350


aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat      11
04
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
         355                 360                 365


tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac      11
52
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
     370                 375                 380


agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act      12
00
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
```

```
385                    390                    395                    400

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag    12
48
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
                  405                    410                    415


aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata    12
96
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
                  420                    425                    430


ctt gct aca gtt tca gtt ttg gct gtt ggc agt ttg gct cca ata tct    13
44
Leu Ala Thr Val Ser Val Leu Ala Val Gly Ser Leu Ala Pro Ile Ser
            435                    440                    445


gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat gga    13
92
Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly
         450                    455                    460


gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt aga    14
40
Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg

465                    470                    475                    480


aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga ttt    14
88
Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe
                  485                    490                    495


atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc aaa    15
36
Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys
```

```
                500                    505                    510

agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa cct      15
84
Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro

          515                    520                    525

gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac aca      16
32
Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr

      530                    535                    540

act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc cac      16
80
Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His

545                    550                    555                    560

aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca tac      17
28
Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr

              565                    570                    575

att gcc caa gaa taa                                                  17
43
Ile Ala Gln Glu

          580


<210>  12
<211>  580
<212>  PRT
<213>  Artificial

<400>  12

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
```

```
1                    5                    10                                   15


Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
            20              25              30


Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
            35              40              45


Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
        50              55              60


Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65                  70              75                      80


Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
                85              90              95


Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
            100             105             110


Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
            115             120             125


Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
        130             135             140


Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145                 150             155                     160


Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
                165             170                     175


Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
            180             185             190


Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
```

```
        195                200                      205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
    210                215                220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225                    230                235                    240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
            245                250                255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
            260                265                270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
        275                280                285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
    290                295                300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305                    310                315                    320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
            325                330                335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
            340                345                350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
        355                360                365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
    370                375                380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
```

```
385                         390                         395                         400
```

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
            405   410   415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
            420   425   430

Leu Ala Thr Val Ser Val Leu Ala Val Gly Ser Leu Ala Pro Ile Ser
        435   440   445

Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly
        450   455   460

Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg
465   470   475   480

Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe
            485   490   495

Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys
            500   505   510

Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro
        515   520   525

Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr
        530   535   540

Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His
545   550   555   560

Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr
            565   570   575

Ile Ala Gln Glu

```
<210>  13
<211>  1746
<212>  DNA
<213>  Artificial

<220>
<223>  Codes for a mutated Human Adenovirus type 5 fiber protein.

<220>
<221>  CDS
<222>  (1)..(1746)

<220>
<221>  mutation
<222>  (1321)..(1326)

<400>  13
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca    48
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1               5                   10                  15


tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc    96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
                20                  25                  30


ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct    1
                                                                    44
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
        35                  40                  45


ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc    1
                                                                    92
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
    50                  55                  60
```

```
aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc      2
40
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65                  70                  75                  80


caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac      2
88
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
                    85                  90                  95


ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta      3
36
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
                100                 105                 110


act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc      3
84
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
        115                 120                 125


atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att      4
32
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
    130                 135                 140


gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa      4
80
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145                 150                 155                 160


aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act      5
28
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
                165                 170                 175
```

```
gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg      5
76
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
            180                 185                 190


aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg      6
24
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
            195                 200                 205


gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act      6
72
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
        210                 215                 220


ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act      7
20
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr

225                 230                 235                 240


gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca      7
68
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
                245                 250                 255


gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt      8
16
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
            260                 265                 270


agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag      8
64
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
            275                 280                 285
```

```
ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac      9
12
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
     290                 295                 300


aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag      9
60
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305                 310                 315                 320


gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata     10
08
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
                 325                 330                 335


gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca     10
56
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
                 340                 345                 350


aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat     11
04
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
             355                 360                 365


tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac     11
52
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
     370                 375                 380


agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act     12
00
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
```

Page 58

```
ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag    12
48
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu

                405                     410                     415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata    12
96
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile

                420                     425                     430

ctt gct aca gtt tca gtt ttg gct gct gca ggc agt ttg gct cca ata    13
44
Leu Ala Thr Val Ser Val Leu Ala Ala Ala Gly Ser Leu Ala Pro Ile

        435                     440                     445

tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat    13
92
Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn

    450                     455                     460

gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt    14
40
Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe

465                     470                     475                     480

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga    14
88
Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly

                485                     490                     495

ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc    15
36
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
```

```
                500                     505                     510


aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa      15
84
Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys

         515                     520                     525


cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac      16
32
Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp

     530                     535                     540


aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc      16
80
Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly

545                     550                     555                     560


cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca      17
28
His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser

              565                     570                     575


tac att gcc caa gaa taa                                              17
46
Tyr Ile Ala Gln Glu

           580



<210>  14
<211>  581
<212>  PRT
<213>  Artificial

<400>  14

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
```

```
1                  5                    10                        15
```

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
              20   25   30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
          35   40   45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
      50   55   60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65   70   75   80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
              85   90   95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
          100   105   110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
          115   120   125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
      130   135   140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145   150   155   160

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
              165   170   175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
          180   185   190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

               195   200   205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
    210   215   220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225   230   235   240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
              245   250   255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
              260   265   270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
          275   280   285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
    290   295   300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305   310   315   320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
              325   330   335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
              340   345   350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
          355   360   365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
    370   375   380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

```
385                    390               395                 400
```

```
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
                405             410               415
```

```
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
            420             425               430
```

```
Leu Ala Thr Val Ser Val Leu Ala Ala Ala Gly Ser Leu Ala Pro Ile
            435             440               445
```

```
Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
        450             455               460
```

```
Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465                 470             475                 480
```

```
Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
                485             490               495
```

```
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
                500             505               510
```

```
Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
            515             520               525
```

```
Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
        530             535               540
```

```
Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
545                 550             555                 560
```

```
His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
            565             570               575
```

```
Tyr Ile Ala Gln Glu
```

580

```
<210>  15
<211>  1746
<212>  DNA
<213>  Artificial

<220>
<223>  Codes for a mutated Human Adenovirus type 5 fiber protein.

<220>
<221>  CDS
<222>  (1)..(1746)

<220>
<221>  mutation
<222>  (1378)..(1380)

<400>  15
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca    48
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1               5                   10                  15


tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc    96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
                20                  25                  30


ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct   144
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
        35                  40                  45


ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc   192
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
    50                  55                  60
```

```
aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc    2
40
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65                  70              75                  80


caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac    2
88
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
                85                  90                  95


ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta    3
36
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
              100                 105                 110


act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc    3
84
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
          115                 120                 125


atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att    4
32
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
      130                 135                 140


gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa    4
80
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145                 150                 155                 160


aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act    5
28
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
              165                 170                 175
```

```
gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg      5
76
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu

            180                185                190


aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg      6
24
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

         195                200                205


gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act      6
72
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr

      210                215                220


ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act      7
20
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr

225                230                235                240


gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca      7
68
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala

            245                250                255


gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt      8
16
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val

         260                265                270


agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag      8
64
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln

      275                280                285
```

```
ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac      9
12
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
    290               295               300


aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag      9
60
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu

305               310               315               320


gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata     10
08
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
              325               330               335


gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca     10
56
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
              340               345               350


aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat     11
04
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
              355               360               365


tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac     11
52
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
    370               375               380


agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act     12
00
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
```

385   390   395   400

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag   12
48
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
                    405   410   415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata   12
96
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
               420   425   430

ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata   13
44
Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
          435   440   445

tct gga aca gtt caa agt gct cat ctt att ata gaa ttc gac gaa aat   13
92
Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Glu Phe Asp Glu Asn
     450   455   460

gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt   14
40
Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465   470   475   480

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga   14
88
Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
               485   490   495

ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc   15
36
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala

```
                500                      505                      510

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa    15
84
Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys

         515                      520                      525

cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac    16
32
Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp

      530                      535                      540

aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc    16
80
Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly

545                      550                      555                      560

cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca    17
28
His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser

               565                      570                      575

tac att gcc caa gaa taa                                            17
46
Tyr Ile Ala Gln Glu

               580
```

```
<210>  16
<211>  581
<212>  PRT
<213>  Artificial

<400>  16

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
```

```
1                    5                    10                              15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
            20                  25              30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
            35                  40              45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
        50                  55              60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65                      70                  75                      80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
            85                  90                  95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
            100                 105                 110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
        115                 120                 125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
        130                 135                 140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145                 150                 155                     160

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
            165                 170                 175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
            180                 185                 190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
```

195   200   205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
    210   215   220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225   230   235   240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
            245   250   255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
            260   265   270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
        275   280   285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
    290   295   300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305   310   315   320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
            325   330   335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
            340   345   350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
        355   360   365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
    370   375   380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

385   390   395   400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
              405   410   415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
              420   425   430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
          435   440   445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Glu Phe Asp Glu Asn
      450   455   460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465   470   475   480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
              485   490   495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
              500   505   510

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
          515   520   525

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
      530   535   540

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
545   550   555   560

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
              565   570   575

Tyr Ile Ala Gln Glu

```
<210>  17
<211>  1740
<212>  DNA
<213>  Artificial

<220>
<223>  Codes for a mutated Human Adenovirus type 5 fiber protein.  Nucle
       otides corresponding to amino acids 509(G) & 510(K) of wild-type
       fiber were deleted

<220>
<221>  CDS
<222>  (1)..(1740)

<400>  17
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca      48
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1               5                   10                  15


tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc      96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
                20                  25                  30


ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct     144
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
            35                  40                  45


ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc     192
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
        50                  55                  60
```

```
aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc      2
40
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65                  70                  75                  80


caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac      2
88
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
                 85                  90                  95


ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta      3
36
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
                100                 105                 110


act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc      3
84
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
        115                 120                 125


atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att      4
32
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
    130                 135                 140


gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa      4
80
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145                 150                 155                 160


aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act      5
28
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
                165                 170                 175
```

```
gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg     5
76
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
            180                 185                 190


aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg     6
24
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
            195                 200                 205


gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act     6
72
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
            210                 215                 220


ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act     7
20
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225                 230                 235                 240


gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca    7
68
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
                245                 250                 255


gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt     8
16
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
            260                 265                 270


agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag     8
64
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
            275                 280                 285
```

```
ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac    9
12
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
    290             295             300


aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag    9
60
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu

305             310             315             320


gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata    10
08
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
            325             330             335


gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca    10
56
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
            340             345             350


aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat    11
04
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
        355             360             365


tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac    11
52
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
    370             375             380


agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act    12
00
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
```

```
ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag   12
48
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
                405                    410                    415


aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata   12
96
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
            420                    425                    430


ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata   13
44
Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
         435                    440                    445


tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat   13
92
Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
      450                    455                    460


gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt   14
40
Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465                    470                    475                    480


aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga   14
88
Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
                485                    490                    495


ttt atg cct aac cta tca gct tat cca aaa tct cac act gcc aaa agt   15
36
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Thr Ala Lys Ser
```

```
                500                      505                    510

aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa cct gta      15
84
Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val

        515                  520                    525

aca cta acc att aca cta aac ggt aca cag gaa aca gga gac aca act      16
32
Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr

      530                  535                    540

cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc cac aac      16
80
Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn

545                  550                    555                    560

tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca tac att      17
28
Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile

              565                  570                    575

gcc caa gaa taa                                                      17
40
Ala Gln Glu
```

```
<210>  18
<211>  579
<212>  PRT
<213>  Artificial

<400>  18

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
```

```
1                    5                    10                                   15
```

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
            20   25   30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
        35   40   45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
    50   55   60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65   70   75   80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
            85   90   95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
            100   105   110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
        115   120   125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
    130   135   140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145   150   155   160

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
            165   170   175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
        180   185   190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

195   200   205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
    210   215   220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225   230   235   240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
            245   250   255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
            260   265   270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
        275   280   285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
    290   295   300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305   310   315   320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
            325   330   335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
            340   345   350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
        355   360   365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
    370   375   380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

```
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
                405             410             415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
            420             425             430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
        435             440             445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
    450             455             460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465             470             475             480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
            485             490             495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Thr Ala Lys Ser
            500             505             510

Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val
        515             520             525

Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr
    530             535             540

Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn
545             550             555             560

Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile
            565             570             575

Ala Gln Glu
```

Page 81

```
<210>   19
<211>   1740
<212>   DNA
<213>   Artificial

<220>
<223>   Codes for a mutated Human Adenovirus type 5 fiber protein.  Nuc
le
        otides corresponding to amino acids 538(G) & 539(T) of wild-typ
e
        fiber were deleted

<220>
<221>   CDS
<222>   (1)..(1740)

<400>   19
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca
48
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1               5                   10                  15


tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc
96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
                20                  25                  30


ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct        1
44
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
        35                  40                  45


ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc        1
92
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
    50                  55                  60
```

```
aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc    2
40
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65                  70                  75                  80


caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac    2
88
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
                85                  90                  95


ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta    3
36
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
             100                 105                 110


act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc    3
84
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
          115                 120                 125


atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att    4
32
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
       130                 135                 140


gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa    4
80
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145                 150                 155                 160


aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act    5
28
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
             165                 170                 175
```

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg   5
76
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
              180   185   190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg   6
24
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
              195   200   205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act   6
72
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
         210   215   220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act   7
20
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225   230   235   240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca   7
68
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
              245   250   255

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt   8
16
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
              260   265   270

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag   8
64
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
              275   280   285

```
ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac        9
12
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn

      290                 295                 300


aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag        9
60
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu

305                 310                 315                 320


gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata        10
08
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile

                  325                 330                 335


gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca       10
56
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro

                  340                 345                 350


aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat       11
04
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp

            355                 360                 365


tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac       11
52
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp

      370                 375                 380


agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act       12
00
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
```

```
     385                     390                      395                          400

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag      12
48
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
                      405                      410                  415


aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata      12
96
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
                420                      425                      430


ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata      13
44
Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
              435                      440                      445


tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat      13
92
Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
          450                      455                      460


gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt      14
40
Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465                      470                      475                      480


aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga      14
88
Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
                485                      490                      495


ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc      15
36
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
```

Page 86

```
                500                    505                        510


aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa       15
84
Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys


         515                    520                    525


cct gta aca cta acc att aca cta aac cag gaa aca gga gac aca act       16
32
Pro Val Thr Leu Thr Ile Thr Leu Asn Gln Glu Thr Gly Asp Thr Thr


      530                    535                    540


cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc cac aac       16
80
Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn

545                    550                    555                    560


tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca tac att       17
28
Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile


                565                    570                    575


                                                                      17
gcc caa gaa taa                                                       40
Ala Gln Glu




<210>  20
<211>  579
<212>  PRT
<213>  Artificial

<400>  20

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
```

```
1                    5                    10                              15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
            20                  25                  30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
            35                  40                  45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
    50                  55                  60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65                  70                  75                          80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
            85                  90                  95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
            100                 105                 110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
            115                 120                 125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
    130                 135                 140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145                 150                 155                         160

Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
            165                 170                 175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
            180                 185                 190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
```

Page 88

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
    210   215   220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225   230   235   240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
            245   250   255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
            260   265   270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
    275   280   285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
    290   295   300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305   310   315   320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
            325   330   335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
            340   345   350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
    355   360   365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
    370   375   380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
                        Page 89

385   390   395   400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
                405   410   415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
            420   425   430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
        435   440   445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
    450   455   460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465   470   475   480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
                485   490   495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
            500   505   510

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
        515   520   525

Pro Val Thr Leu Thr Ile Thr Leu Asn Gln Glu Thr Gly Asp Thr Thr
    530   535   540

Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn
545   550   555   560

Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile
            565   570   575

Ala Gln Glu

```
<210>  21
<211>  38
<212>  DNA
<213>  Artificial

<220>
<223>  PCR primer

<220>
<221>  primer_bind
<222>  (1)..(38)

<400>  21
accacaccag ctccagaggc taactgtaga ctaaatgc
38


<210>  22
<211>  38
<212>  DNA
<213>  Artificial

<220>
<223>  PCR primer

<220>
<221>  primer_bind
<222>  (1)..(38)

<400>  22
gcatttagtc tacagttagc ctctggagct ggtgtgtt
38


<210>  23
<211>  38
<212>  DNA
<213>  Artificial

<220>
<223>  PCR primer

<220>
<221>  primer_bind
<222>  (1)..(38)
```

Page 91

```
<400>  23
acagtttcag ttttggccgg cagtttggct ccaatatc
38


<210>  24
<211>  38
<212>  DNA
<213>  Artificial

<220>
<223>  PCR primer

<220>
<221>  primer_bind
<222>  (1)..(38)

<400>  24
gatattggag ccaaactgcc ggccaaaact gaaactgt
38


<210>  25
<211>  36
<212>  DNA
<213>  Artificial

<220>
<223>  PCR primer

<220>
<221>  primer_bind
<222>  (1)..(36)

<400>  25
acagtttcag ttttggctaa aggcagtttg gctcca
36


<210>  26
<211>  36
<212>  DNA
<213>  Artificial

<220>
<223>  PCR primer
```

<220>
<221> primer_bind
<222> (1)..(36)

<400> 26
tggagccaaa ctgcctttag ccaaaactga aactgt
36

<210> 27
<211> 36
<212> DNA
<213> Artificial

<220>
<223> PCR primer

<220>
<221> primer_bind
<222> (1)..(36)

<400> 27
gtttcagttt tggctgttgg cagtttggct ccaata
36

<210> 28
<211> 36
<212> DNA
<213> Artificial

<220>
<223> PCR primer

<220>
<221> primer_bind
<222> (1)..(36)

<400> 28
tattggagcc aaactgccaa cagccaaaac tgaaac
36

<210> 29
<211> 36
<212> DNA
<213> Artificial

```
<220>
<223>  PCR primer

<220>
<221>  primer_bind
<222>  (1)..(36)

<400>  29
gtttcagttt tggctgctgc aggcagtttg gctcca
36


<210>  30
<211>  36
<212>  DNA
<213>  Artificial

<220>
<223>  PCR primer

<220>
<221>  primer_bind
<222>  (1)..(36)

<400>  30
tggagccaaa ctgcctgcag cagccaaaac tgaaac
36


<210>  31
<211>  36
<212>  DNA
<213>  Artificial

<220>
<223>  PCR primer

<220>
<221>  primer_bind
<222>  (1)..(36)

<400>  31
gctcatctta ttatagaatt cgacgaaaat ggagtg
36


<210>  32
<211>  36
```

```
<212>  DNA
<213>  Artificial

<220>
<223>  PCR primer

<220>
<221>  primer_bind
<222>  (1)..(36)

<400>  32
cactccattt tcgtcgaatt ctataataag atgagc
36


<210>  33
<211>  39
<212>  DNA
<213>  Artificial

<220>
<223>  PCR primer

<220>
<221>  primer_bind
<222>  (1)..(39)

<400>  33
gcttatccaa aatctcacac tgccaaaagt aacattgtc
39


<210>  34
<211>  39
<212>  DNA
<213>  Artificial

<220>
<223>  PCR primer

<220>
<221>  primer_bind
<222>  (1)..(39)

<400>  34
gacaatgtta cttttggcag tgtgagattt tggataagc
39
```

```
<210>  35
<211>  35
<212>  DNA
<213>  Artificial

<220>
<223>  PCR primer

<220>
<221>  primer_bind
<222>  (1)..(35)

<400>  35
ctaaccatta cactaaacca ggaaacagga gacac
35


<210>  36
<211>  35
<212>  DNA
<213>  Artificial

<220>
<223>  PCR primer

<220>
<221>  primer_bind
<222>  (1)..(35)

<400>  36
gtgtctcctg tttcctggtt tagtgtaatg gttag
35


<210>  37
<211>  33
<212>  DNA
<213>  Artificial

<220>
<223>  PCR primer

<220>
<221>  primer_bind
<222>  (1)..(33)

<400>  37
```

Page 96

```
ataagatttg acgaaactgg agtgctacta aac
33
```

```
<210>   38
<211>   33
<212>   DNA
<213>   Artificial

<220>
<223>   PCR primer

<220>
<221>   primer_bind
<222>   (1)..(33)

<400>   38
gtttagtagc actccagttt cgtcaaatct tat
33
```

```
<210>   39
<211>   33
<212>   DNA
<213>   Artificial

<220>
<223>   PCR primer

<220>
<221>   primer_bind
<222>   (1)..(33)

<400>   39
tttgacgaaa atggacacct actaaacaat tcc
33
```

```
<210>   40
<211>   33
<212>   DNA
<213>   Artificial

<220>
<223>   PCR primer

<220>
<221>   primer_bind
```

```
<222>  (1)..(33)

<400>  40
ggaattgttt agtaggtgtc cagtttcgtc aaa
33


<210>  41
<211>  33
<212>  DNA
<213>  Artificial

<220>
<223>  PCR primer

<220>
<221>  primer_bind
<222>  (1)..(33)

<400>  41
aacctatcag cttatgcaaa atctcacggt aaa
33


<210>  42
<211>  32
<212>  DNA
<213>  Artificial

<220>
<223>  PCR primer

<220>
<221>  primer_bind
<222>  (1)..(32)

<400>  42
tttaccgtga gattttgcat aagctgatag gt
32


<210>  43
<211>  10
<212>  PRT
<213>  Artificial

<220>
<223>  cRGD consensus sequence
```

Page 98

<400> 43

His Cys Asp Cys Arg Gly Asp Cys Phe Cys
1   5   10